

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: CIBA-GEIGY AG
- (B) STREET: Klybeckstr. 141
- (C) CITY: Basel
- (E) COUNTRY: Switzerland
- (F) POSTAL CODE (ZIP): 4002
- (G) TELEPHONE: +41 61 69 11 11
- (H) TELEFAX: + 41 61 696 79 76
- (I) TELEX: 962 991

(ii) TITLE OF INVENTION: New process for the production of
biologically active protein

(iii) NUMBER OF SEQUENCES: 12

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: E. coli LC137/pPLMu.hTGF-beta1 (DSM 5656)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..336

(D) OTHER INFORMATION:/product= "human TGF-beta1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GCC CTG GAC ACC AAC TAT TGC TTC AGC TCC ACG GAG AAG AAC TGC TGC	48
Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys	
1 5 10 15	
GTG CGG CAG CTG TAC ATT GAC TTC CGC AAG GAC CTC GGC TGG AAG TGG	96
Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp	
20 25 30	
ATC CAC GAG CCC AAG GGC TAC CAT GCC AAC TTC TGC CTC GGG CCC TGC	144
Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys	
35 40 45	
CCC TAC ATT TGG AGC CTG GAC ACG CAG TAC AGC AAG GTC CTG GCC CTG	192
Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu	
50 55 60	
TAC AAC CAG CAT AAC CCG GGC GCC TCG GCG GCG CCG TGC TGC GTG CCG	240
Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro	
65 70 75 80	
CAG GCG CTG GAG CCG CTG CCC ATC GTG TAC TAC GTG GGC CGC AAG CCC	288

Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro
85 90 95

AAG GTG GAG CAG CTG TCC AAC ATG ATC GTG CGC TCC TGC AAG TGC AGC 336
Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
100 105 110

TGA 339

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys
1 5 10 15

Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp
20 25 30

Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys
35 40 45

Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu
50 55 60

Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro
65 70 75 80

Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro
85 90 95

Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser

100

105

110

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: E. coli LC137/pPLMu.hTGF-beta2 (DSM5657)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..336

(D) OTHER INFORMATION:/product= "human TGF-beta2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCT TTG GAT GCG GCC TAT TGC TTT AGA AAT GTG CAG GAT AAT TGC TGC 48

Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys

115

120

125

CTA CGT CCA CTT TAC ATT GAT TTC AAG AGG GAT CTA GGG TGG AAA TGG 96

Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp

130

135

140

ATA CAC GAA CCC AAA GGG TAC AAT GCC AAC TTC TGT GCT GGA GCA TGC 144

Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	

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Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys
35 40 45

Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu Ser Leu
50 55 60

Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser
65 70 75 80

Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Lys Thr Pro
85 90 95

Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser
100 105 110

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: E. coli LC137/pPLMu.hTGF-beta3 (DSM 5658)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..336
- (D) OTHER INFORMATION: /product= "human TGF-beta3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GCT TTG GAC ACC AAT TAC TGC TTC CGC AAC TTG GAG GAG AAC TGC TGT	48
Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys	
115 120 125	
GTG CGC CCC CTC TAC ATT GAC TTC CGA CAG GAT CTG GGC TGG AAG TGG	96
Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp	
130 135 140	
GTC CAT GAA CCT AAG GGC TAC TAT GCC AAC TTC TGC TCA GGC CCT TGC	144
Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys	
145 150 155 160	
CCA TAC CTC CGC AGT GCA GAC ACA ACC CAC AGC ACG GTG CTG GGA CTG	192
Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu	
165 170 175	
TAC AAC ACT CTG AAC CCT GAA GCA TCT GCC TCG CCT TGC TGC GTG CCC	240
Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro	
180 185 190	
CAG GAC CTG GAG CCC CTG ACC ATC CTG TAC TAT GTT GGG AGG ACC CCC	288
Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro	
195 200 205	
AAA GTG GAG CAG CTC TCC AAC ATG GTG GTG AAG TCT TGT AAA TGT AGC	336
Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser	
210 215 220	
TGA	339

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys
1 5 10 15

Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp
20 25 30

Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys
35 40 45

Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu
50 55 60

Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro
65 70 75 80

Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro
85 90 95

Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser
100 105 110

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "recombinant hybrid DNA of

TGF-beta1 and TGF-beta3 DNA"

(vii) IMMEDIATE SOURCE:

(B) CLONE: E. coli LC137/pPLMu.TGF-beta1(44/45)beta3

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION:1..132

(D) OTHER INFORMATION:/product= "N-terminal 44 amino acids of human TGF-beta1"

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION:133..336

(D) OTHER INFORMATION:/product= "C-terminal 68 amino acids of human TGF-beta3"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..336

(D) OTHER INFORMATION:/product= "hybrid TGF-beta named TGF-beta1-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCC CTG GAC ACC AAC TAT TGC TTC AGC TCC ACG GAG AAG AAC TGC TGC	48
Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys	
1 5 10 15	
GTG CGG CAG CTG TAC ATT GAC TTC CGC AAG GAC CTC GGC TGG AAG TGG	96
Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp	
20 25 30	
ATC CAC GAG CCC AAG GGC TAC CAT GCC AAC TTC TGC TCA GGC CCT TGC	144
Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Ser Gly Pro Cys	

35	40	45	
CCA TAC CTC CGC AGT GCA GAC ACA ACC CAC AGC ACG GTG CTG GGA CTG			192
Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu			
50	55	60	
TAC AAC ACT CTG AAC CCT GAA GCA TCT GCC TCG CCT TGC TGC GTG CCC			240
Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro			
65	70	75	80
CAG GAC CTG GAG CCC CTG ACC ATC CTG TAC TAT GTT GGG AGG ACC CCC			288
Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro			
85	90	95	
AAA GTG GAG CAG CTC TCC AAC ATG GTG GTG AAG TCT TGT AAA TGT AGC			336
Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser			
100	105	110	

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys			
1	5	10	15
Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp			
20	25	30	
Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Ser Gly Pro Cys			
35	40	45	

Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu

50

55

60

Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro

65

70

75

80

Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro

85

90

95

Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser

100

105

110

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "recombinant hybrid DNA
coding for hybrid TGF-beta2-3"

(vii) IMMEDIATE SOURCE:

(B) CLONE: E. coli LC137/pPLMu.TGF-beta2(44/45)beta3

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION:1..132

(D) OTHER INFORMATION:/product= "N-terminal 44 amino
acids of human TGF-beta2"

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION:133..336
 (D) OTHER INFORMATION:/product= "C-terminal 68 amino acids of human TGF-beta3"

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION:1..336
 (D) OTHER INFORMATION:/product= "hybrid TGF-beta2-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GCT TTG GAT GCG GCC TAT TGC TTT AGA AAT GTG CAG GAT AAT TGC TGC	48
Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys	
1 5 10 15	
CTA CGT CCA CTT TAC ATT GAT TTC AAG AGG GAT CTA GGG TGG AAA TGG	96
Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp	
20 25 30	
ATA CAC GAA CCC AAA GGG TAC AAT GCC AAC TTC TGC TCA GGC CCT TGC	144
Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ser Gly Pro Cys	
35 40 45	
CCA TAC CTC CGC AGT GCA GAC ACA ACC CAC AGC ACG GTG CTG GGA CTG	192
Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu	
50 55 60	
TAC AAC ACT CTG AAC CCT GAA GCA TCT GCC TCG CCT TGC TGC GTG CCC	240
Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro	
65 70 75 80	
CAG GAC CTG GAG CCC CTG ACC ATC CTG TAC TAT GTT GGG AGG ACC CCC	288
Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro	
85 90 95	

AAA GTG GAG CAG CTC TCC AAC ATG GTG GTG AAG TCT TGT AAA TGT AGC 336
Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser
100 105 110

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys
1 5 10 15
Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp
20 25 30
Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ser Gly Pro Cys
35 40 45
Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu
50 55 60
Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro
65 70 75 80
Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro
85 90 95
Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser
100 105 110

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "recombinant hybrid DNA coding for hybrid TGF-beta3-2"

(vii) IMMEDIATE SOURCE:

(B) CLONE: E. coli LC137/pPLMu.TGF-beta3(44/45)beta2

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:1..132
- (D) OTHER INFORMATION:/product= "N-terminal 44 amino acids of human TGF-beta3"

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:133..336
- (D) OTHER INFORMATION:/product= "C-terminal 68 amino acids of human TGF-beta2"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..336
- (D) OTHER INFORMATION:/product= "hybrid TGF-beta3-2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCT TTG GAC ACC AAT TAC TGC TTC CGC AAC TTG GAG GAG AAC TGC TGT

Ala	Leu	Asp	Thr	Asn	Tyr	Cys	Phe	Arg	Asn	Leu	Glu	Glu	Asn	Cys	Cys		
1				5					10					15			
GTG	CGC	CCC	CTC	TAC	ATT	GAC	TTC	CGA	CAG	GAT	CTG	GGC	TGG	AAG	TGG	96	
Val	Arg	Pro	Leu	Tyr	Ile	Asp	Phe	Arg	Gln	Asp	Leu	Gly	Trp	Lys	Trp		
			20					25					30				
GTC	CAT	GAA	CCT	AAG	GGC	TAC	TAT	GCC	AAC	TTC	TGT	GCT	GGA	GCA	TGC	144	
Val	His	Glu	Pro	Lys	Gly	Tyr	Tyr	Ala	Asn	Phe	Cys	Ala	Gly	Ala	Cys		
			35					40					45				
CCG	TAT	TTA	TGG	AGT	TCA	GAC	ACT	CAG	CAC	AGC	AGG	GTC	CTG	AGC	TTA	192	
Pro	Tyr	Leu	Trp	Ser	Ser	Asp	Thr	Gln	His	Ser	Arg	Val	Leu	Ser	Leu		
			50					55				60					
TAT	AAT	ACC	ATA	AAT	CCA	GAA	GCA	TCT	GCT	TCT	CCT	TGC	TGC	GTG	TCC	240	
Tyr	Asn	Thr	Ile	Asn	Pro	Glu	Ala	Ser	Ala	Ser	Pro	Cys	Cys	Val	Ser		
			65			70				75					80		
CAA	GAT	TTA	GAA	CCT	CTA	ACC	ATT	CTC	TAC	TAC	ATT	GGC	AAA	ACA	CCC	288	
Gln	Asp	Leu	Glu	Pro	Leu	Thr	Ile	Leu	Tyr	Tyr	Ile	Gly	Lys	Thr	Pro		
						85				90				95			
AAG	ATT	GAA	CAG	CTT	TCT	AAT	ATG	ATT	GTA	AAG	TCT	TGC	AAA	TGC	AGC	336	
Lys	Ile	Glu	Gln	Leu	Ser	Asn	Met	Ile	Val	Lys	Ser	Cys	Lys	Cys	Ser		
						100				105				110			

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys

1

5

10

15

Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp

20

25

30

Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ala Gly Ala Cys

35

40

45

Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu Ser Leu

50

55

60

Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser

65

70

75

80

Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Lys Thr Pro

85

90

95

Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser

100

105

110